FIGURE 1A

```
                    10        20        30        40        50        60
                     |         |         |         |         |         |
serotype f  MNQKIVVISSFYMLGAHSFSKAVYHNDRSVKLMKRIDINHQAQRFSIRKYAFGAASVLIG
                                            ****************************
serotype c  --------------------------------MKRIDINHQAQRFSIRKYAFGAASVLIG

                    70        80        90       100       110       120
                     |         |         |         |         |         |
serotype f  CVFFLGTQNVSAQEQGTQLPASENAVVNVAENSVAISQAVADKAATQTTLTETPQVEVEE
            ****************************************:****:**************
serotype c  CVFFLGTQNVSAQEQGTQLPASENAVVNVAENSVAISQAVSDKAAAQTTLTETPQVEVEE

                   130       140       150       160       170       180
                     |         |         |         |         |         |
serotype f  KESKVNAPALNVDDKGAKSKEDVNPTISKTASEVEASAVTATDTKNSNPQVNVETDSSEK
            **.************************:******************************.**
serotype c  KENKVNAPALNVDDKGAKSKEDVNPTVSKTASEVEASAVTATDTKNSNPQVNVETDSNEK

                   190       200       210       220       230       240
                     |         |         |         |         |         |
serotype f  DENKMVTSAPAKETEAEQNEKAVRENLMQRQAKAVSIPSQGNYVFQETTPVKNAASMSSP
            *********************** ***MSRQAKAVNIP******************MQSP
serotype c  DENKMVTSAPAKETEAEQNEKAVAENLMQRQAKAVSIPSQGNYVFQETTPVKNAASMSSP

                   250       260       270       280       290       300
                     |         |         |         |         |         |
serotype f  TQFNFDKGDKVFYDNVLEADGHQWISYVSYSGIRRYAPIAVTIEELKQKEIVQQNLPAQG
            TEFNEDK*******:*********************************************
serotype c  TQFNFDKGDKVFYDKVLEADGHQWISYVSYSGIRRYAPIAVTIEELKQKEIVQQNLPAQG

                   310       320       330       340       350       360
                     |         |         |         |         |         |
serotype f  TYHFTKQQSLK--MKLN-----------------CLVRPNSRFTTEITFFMIRF------
            ******* .:*   **.                  *   . :: : :::  **
serotype c  TYHFTKQADVKNEAKLSSPTQFSFYNGDHVFYDKVLEADGHQWISYVSYSGIRRYVVIGK

                   370       380       390       400       410       420
                     |         |         |         |         |         |
serotype f  ------------------------------------------------------------
serotype c  LTTQPSPIETKVSGTIAIQNKTAQQFDVIISNVSSTQGIKEVLVPVWSEQNGQDDIVWYQ

                   430       440       450       460       470       480
                     |         |         |         |         |         |
serotype f  ------------------------------------------------------------
serotype c  ATKQGEGVYKVTVKVSDHKNNSGNYDIHLYYRLSTGELKVVGGKTTEVEAPKPVETTGII

                   490       500       510       520       530       540
                     |         |         |         |         |         |
serotype f  ------------------------------------------------------------
serotype c  SIANKSSQGFDVLITNASSTQGIKEVLVPVWSEQNGQDDIIWYQATKQGEGVYKVTVKVS

                   550       560       570       580       590       600
                     |         |         |         |         |         |
serotype f  ------------------------------------------------------------
serotype c  DHKNDSGNYDIHLYYRLSTGELKVVGGKTTTVEAPNRVNLPAQGTYVFTNKVEVKNEART

                   610       620       630       640
                     |         |         |         |
serotype f  ------------------------------------------
serotype c  SSPTQFTFNKGESIYYDSILNADGHQWISYRSYSGIRRYIIID
```

FIGURE 1B

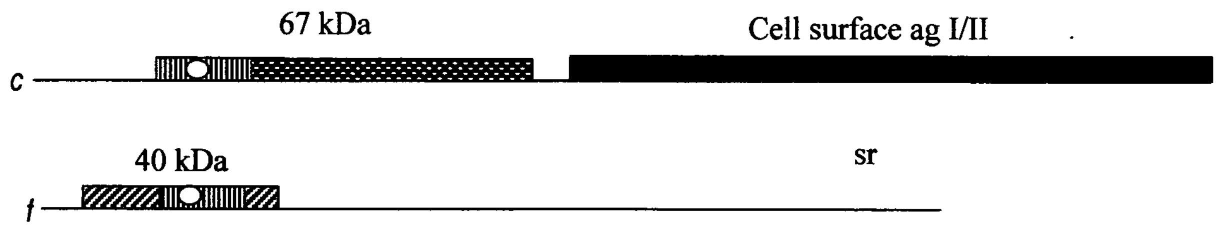


FIGURE 2A

```
                  10        20        30        40
                   |         |         |         |
65-1s     VKNAASMSSPTQFNFDKGDKVFYDKVLEADGHQWISYVSYSGIRRY
40-1s     VKNAASMSSPTQFNFDKGDKVFYDNVLEADGHQWISYVSYSGIRRY
65-2s     VKNEAKLSSPTQFSFYNGDHVFYDKVLEADGHQWISYVSYSGIRRY
65-3s     VKNEARTSSPTQFTFNKGESIYYDSILNADGHQWISYRSYSGIRRY
Bsp-2s    VKNEAKVASPTQFTLDKGDRIFYDQILTIEGNQWLSYKSFNGVRRF
Bsp-3s    --KEAKISSQTQFTLEKGDKINYDQVLTADGYQWISYKSYSGVRRY
Bsp-4s    VKSQPKVSSPVEFNFQKGEKIHYDQVLVVDGHQWISYKSYSGIRRY
Bsp-1s    VKNTPSKSAPVAFYAKKGDKVFYDQVFNKDNVKWISYKSFCGVRRY
            . .  :: . *   :*: : **.::  :. :*:** *: *:**:

SH3b      VRNSPGTSSPIIGTLKKGDKVKVLGVDG....DWADITYGSGQRGY
          * *    ***      ****     *       *       * * *
```

FIGURE 2B

```
                  10        20        30        40        50        60
                   |         |         |         |         |         |
65-1L     QQFDVIISNVSSTQGIKEVLVPVWSEQNGQDDIVWYQATKQGEGVYKVTVKVSDHKNNSG
65-2L     QGFDVLITNASSTQGIKEVLVPVWSEQNGQDDIIWYQATKQGEGVYKVTVKVSDHKNDSG
Bsp-L     -GFDILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTTGDGNYKVAVSFADHKNEKG
            **::*:* .. :**  * ****:**.***** ** *.. *:* ***:*..:****:.*

                  70        80
                   |         |
65-1L     NYDIHLYYRLSTGELKVVGGKTTEVEAP
65-2L     NYDIHLYYRLSTGELKVVGGKTTTVEAP
Bsp-L     LYNIHLYYQEASGTLVGVTGTKVTVAGT
           *:*****: ::* *  * *... * ..
```

```
c    ----------------------------------------------------------------------------------------------------
f    ATAGTAAAAATTTTTCAAAAAATATATTACGTAAGTATTGCTAAATATTTCTTTTGTGTTTCAATATAGGTGAAAAAAGAAAATGAAGGAAGATTATGAA
              10        20        30        40        50        60        70        80        90       100

                                                                                                1
c    -------------------------------------------------------------------------------------------ATGAAAAGA
f    TCAAAAAATAGTCGTCATTTCGTCATTTTACATGTTAGGTGCTCATTCATTTTCAAAGGCAGTATATCATAATGATAGGAGTGTGAAACTTATGAAAAGA
             110       120       130       140       150       160       170       180       190       200

     10        20        30        40        50        60        70        80        90        100
c    ATTGATATTAATCATCAAGCACAACGTTTTTCTATTCGCAAATATGCATTTGGAGCTGCATCTGTTTTAATTGGCTGTGTCTTTTTTCTAGGTACCCAAA
                                             *
f    ATTGATATTAATCATCAAGCACAACGTTTTTCTATTCGTAAATATGCATTTGGAGCTGCATCTGTTTTAATTGGCTGTGTCTTTTTTCTAGGTACCCAAA
             210       220       230       240       250       260       270       280       290       300

     110       120       130       140       150       160       170       180       190       200
c    ATGTTTCTGCACAAGAGCAGGGAACTCAATTGCCAGCAAGTGAAAACGCAGTTGTGAACGTGGCTGAAAATTCAGTTGCTATCAGCCAAGCAGTTTCAGA

f    ATGTTTCTGCACAAGAGCAGGGAACTCAATTGCCAGCAAGTGAAAACGCAGTTGTGAACGTGGCTGAAAATTCAGTTGCTATCAGCCAAGCAGTTGCAGA
             310       320       330       340       350       360       370       380       390       400

     210       220       230       240       250       260       270       280       290       300
c    TAAGGCAGCAGCTCAAACAACTCTAACAGAAACACCCCAAGTTGAAGTTGAGGAGAAAGAAAATAAGGTAAATGCTCCTGCTTTAAATGTCGATGACAAA

f    TAAGGCAGCAACTCAAACAACTCTAACAGAAACACCCCAAGTTGAAGTTGAGGAGAAAGAAAGTAAGGTAAATGCTCCTGCTTTAAATGTCGATGACAAA
             410       420       430       440       450       460       470       480       490       500

     310       320       330       340       350       360       370       380       390       400
c    GGTGCAAAATCCAAAGAAGATGTGAACCCTACTGTTTCAAAGACAGCAAGTGAAGTGGAAGCTTCTGCAGTAACTGCTACTGATACTAAAAATTCAAATC

f    GGTGCAAAATCCAAAGAAGATGTGAACCCTACTATTTCAAAGACAGCAAGTGAAGTGGAAGCTTCTGCAGTAACTGCTACTGATACTAAAAATTCAAATC
             510       520       530       540       550       560       570       580       590       600

     410       420       430       440       450       460       470       480       490       500
c    CACAAGTCAATGTTGAAACTGACTCAAATGAAAAAGACGAAAATAAAATGGTCACCTCGGCTCCAGCTAAGGAGACTGAGGCAGAACAAAATGAGAAAGC

f    CACAAGTCAATGTTGAAACTGACTCAAGTGAAAAAGACGAAAATAAAATGGTCACCTCGGCTCCAGCTAAGGAGACTGAGGCAGAACAAAATGAGAAAGC
             610       620       630       640       650       660       670       680       690       700

     510       520       530       540       550       560       570       580       590       600
c    GGTAGCAGAAAATCTTATGCAAAGACAAGCTAAGGCTGTCTCAATTCCATCGCAAGGCAATTATGTTTTCCAAGAAACAACTCCTGTAAAAAATGCAGCC
        ***
f    GGTCAGAGAAAATCTTATGCAAAGACAAGCTAAGGCTGTCTCAATTCCATCGCAAGGCAATTATGTTTTCCAAGAAACAACTCCTGTAAAAAATGCAGCC
             710       720       730       740       750       760       770       780       790       800

     610       620       630       640       650       660       670       680       690       700
c    AGTATGTCCAGCCCAACCCAATTTAACTTTGATAAAGGAGATAAGGTTTTTTATGATAAGGTTTTAGAAGCGGATGGGCATCAATGGATTAGCTATGTGT

f    AGTATGTCCAGCCCAACCCAATTTAACTTTGATAAAGGAGATAAGGTTTTTTATGATAATGTTTTAGAAGCGGATGGGCATCAATGGATTAGCTATGTGT
             810       820       830       840       850       860       870       880       890       900

     710       720       730       740       750       760       770       780       790       800
c    CTTACAGTGGTATTCGTCGCTATGCTCCTATTGCTGTGACAATTGAAGAATTGAAGCAAAAAGAAATTGTTCAGCAAAATTTACCGGCACAAGGAACCTA

f    CTTACAGTGGTATTCGTCGCTATGCTCCTATTGCTGTGACAATTGAAGAATTGAAGCAAAAAGAAATTGTTCAGCAAAATTTACCGGCACAAGGAACCTA
             910       920       930       940       950       960       970       980       990      1000
```

FIGURE 3

```
    810       820       830       840       850       860       870       880       890       900
c   TCACTTTACTAAACAAGCAGACGTTAAAAATGAAGCTAAACTGTCTAGTCCGACCCAATTCTCGTTTACAACGGAGATCACGTTTTTTATGATAAGGTT
                   *     **
f   TCACTTTACTAAACA-GCAGAGCTTAAAAATGAAGCTAAACTGTCTAGTCCGACCCAATTCTCGTTTACAACGGAGATCACGTTTTTTATGATAAGGTT
          1010      1020      1030      1040      1050      1060      1070      1080      1090      1100

    910       920       930       940       950       960       970       980       990       1000
c   TTAGAAGCGGATGGGCATCAATGGATTAGCTATGTGTCCTACAGTGGTATCCGTCGTTATGTTGTTATTGGAAAGCTTACGACACAACCCTCTCCAATTG
                  *
f   TTAGAAGCGGATGGACATCAATGGATTAGCTATGTGTCCTACAGTGGTATCCGTCGTTATGTTGTTATTGGAAAGCTTACGACACAACCCTCTCCAATTG
          1110      1120      1130      1140      1150      1160      1170      1180      1190      1200

    1010      1020      1030      1040      1050      1060      1070      1080      1090      1100
c   AAACTAAAGTATCAGGTACTATTGCCATCCAAAATAAAACGGCTCAACAATTCGATGTTATCATTTCTAATGTTTCCAGCACTCAAGGCATAAAAGAGGT
                            *                                  *            *   *    *
f   AAACTAAAGTATCAGGTACTATTGTCATCCAAAATAAAACGGCTCAACAATTCGATGTTGTCATTTCTAATGCTTCAAGCAATCAAGGCATAAAAGAGGT
          1210      1220      1230      1240      1250      1260      1270      1280      1290      1300

    1110      1120      1130      1140      1150      1160      1170      1180      1190      1200
c   ATTAGTGCCGGTTTGGTCAGAGCAAAACGGGCAGGATGACATTGTCTGGTATCAAGCAACTAAACAAGGCGAAGGCGTTTATAAGGTGACCGTTAAGGTC
                                                               **        *
f   ATTAGTGCCAGTTTGGTCAGAGCAAAACGGGCAGGATGACATTGTCTGGTATCAAGCAATCAAACAAGGTGAAGGCGTTTATAAGGTGACCGTTAAGGTC
          1310      1320      1330      1340      1350      1360      1370      1380      1390      1400

    1210      1220      1230      1240      1250      1260      1270      1280      1290      1300
c   AGTGACCATAAAAATAACAGTGGTAACTATGACATTCACCTTTATTATCGCCTTTCAACTGGTGAATTAAAGGTTGTTGGAGGAAAGACAACTGAGGTGG
                     *  *         * ** *  *          *** **** *       **  ** **  *  * *  ** **
f   AGTGACCATAAAAATAATAGCGGTAACTATCATGTCCATCTTTATTATCTTTTGGATAATGGTGAACAAAGAGGAGTCGGGGCAACAATGACTGAGGTGG
          1410      1420      1430      1440      1450      1460      1470      1480      1490      1500

    1310      1320      1330      1340      1350      1360      1370      1380      1390      1400
c   AAGCACCGAAGCCTGTAGAAACAACAGGTATCATTAGCATTGCCAATAAGAGCAGCCAAGGATTTGATGTTTTGATTACTAATGCTTCCAGCACTCAAGG
           **                                                                                          *
f   AAGCACCAGAGCCTGTAGAAACAACAGGTATCATTAGCATTGCCAATAAGAGCAGCCAAGGATTTGATGTTTTGATTACTAATGCTTCCAGCACTCAAGA
          1510      1520      1530      1540      1550      1560      1570      1580      1590      1600

    1410      1420      1430      1440      1450      1460      1470      1480      1490      1500
c   CATAAAAGAGGTATTAGTGCCAGTTTGGTCAGAACAAAACGGACAGGACGATATTATTTGGTATCAAGCAACTAAACAAGGCGAAGGCGTTTATAAGGTG
                *        *
f   CATAAAAGAGGTTTTAGTGCCGGTTTGGTCAGAACAAAACGGACAGGACGATATTATTTGGTATCAAGCAACTAAACAAGGCGAAGGCGTTTATAAGGTG
          1610      1620      1630      1640      1650      1660      1670      1680      1690      1700

    1510      1520      1530      1540      1550      1560      1570      1580      1590      1600
c   ACCGTTAAGGTCAGTGACCATAAAAATGACAGTGGTAACTATGACATTCACCTTTATTATCGCCTTTCAACTGGTGAATTAAAGGTTGTTGGAGGAAAGA
    *                                         *                       **
f   GCCGTTAAGGTCAGTGACCATAAAAATGACAGTGGTAACTATAACATTCACCTTTATTATCGCCTTGTAACTGGTGAATTAAAGGTTGTTGGAGGAAAGA
          1710      1720      1730      1740      1750      1760      1770      1780      1790      1800

    1610      1620      1630      1640      1650      1660      1670      1680      1690      1700
c   CAACGACAGTAGAAGCCCCTAATAGAGTCAATCTTCCAGCACAAGGAACTTATGTTTTCACTAATAAAGTTGAGGTTAAAAATGAGGCCAGAACATCTAG
                               *
f   CAACGACAGTAGAAGCCCCTAATAGAG-CAATCTTCCAGCACAAGGAACTTATGTTTTCACTAATAAAGTTGAGGTTAAAAATGAGGCCAGAACATCTAG
          1810      1820      1830      1840      1850      1860      1870      1880      1890      1900

    1710      1720      1730      1740      1750      1760      1770      1780      1790      1800
c   TCCAACTCAGTTTACCTTTAATAAAGGAGAAAGTATTTACTATGACAGTATCTTGAATGCTGATGGACATCAATGGATTAGCTATCGTTCCTACAGTGGT
f   TCCAACTCAGTTTACCTTTAATAAAGGAGAAAGTATTTACTATGACAGTATCTTGAATGCTGATGGACATCAATGGATTAGCTATCGTTCCTACAGTGGT
          1910      1920      1930      1940      1950      1960      1970      1980      1990      2000

    1810      1820      1830
c   ATTCGTCGTTATATTATCATTGATTGA
                          *
f   ATTCGTCGTTATATTATCATTGGTTGA
             2010      2020
```

FIGURE 3, CTD.

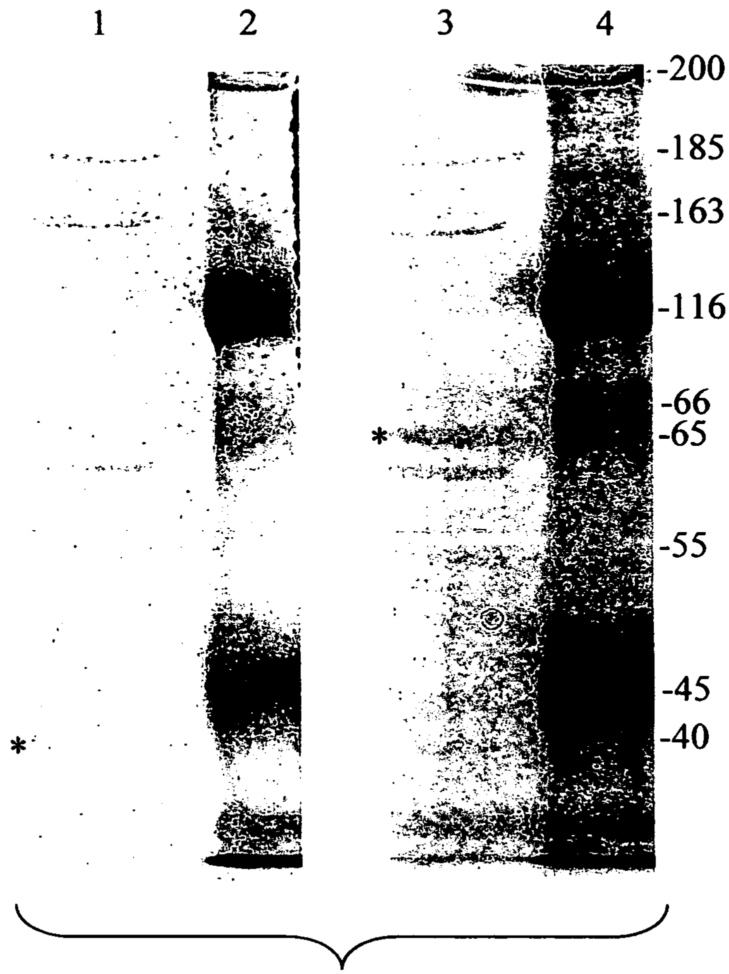


FIGURE 4

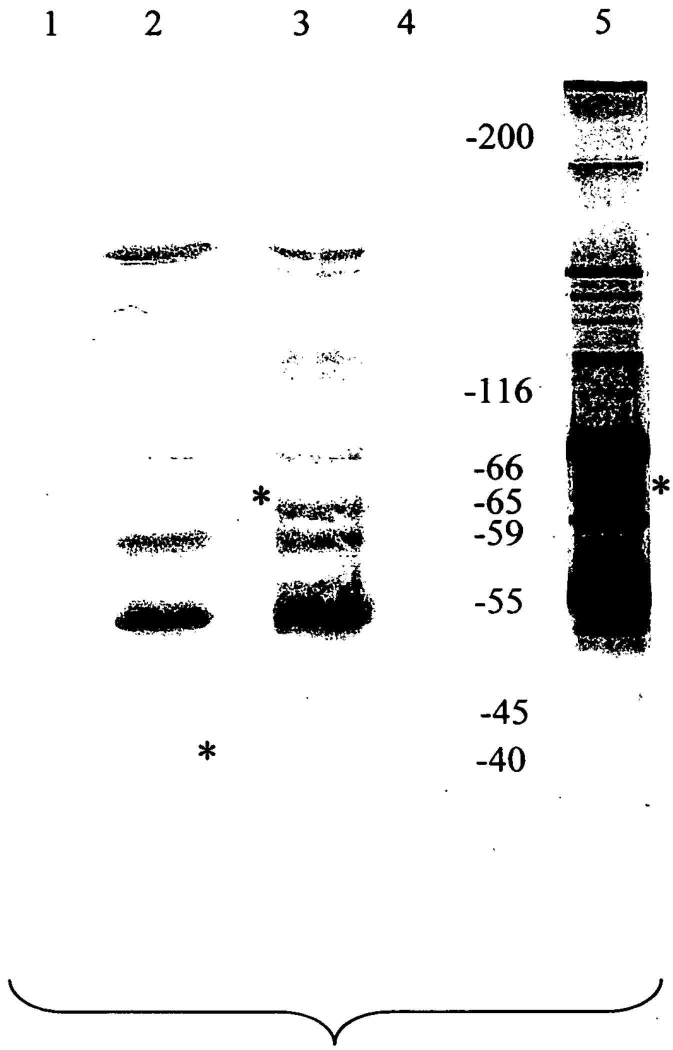
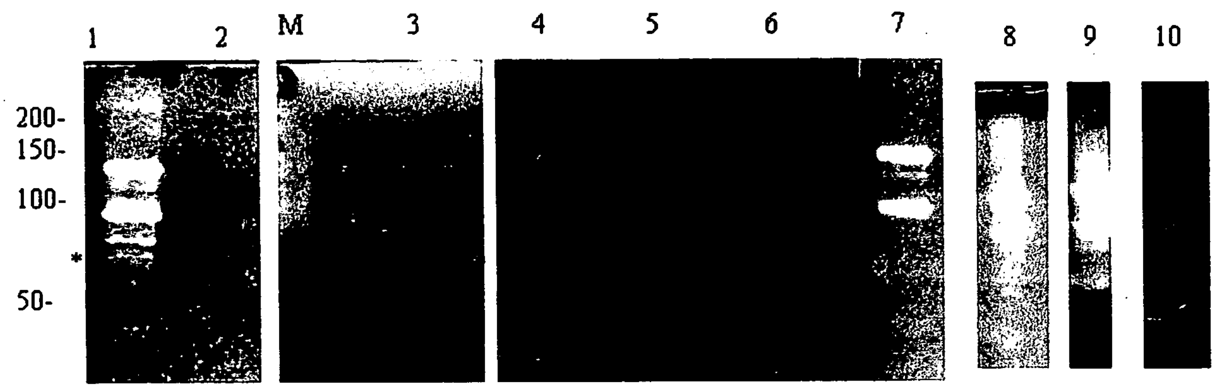


FIGURE 5

Comparison of peptidoglycan source and enzyme source for hydrolytic activity



Enzyme source

OMZ175 peptidoglycan: Lane 1 – A32-2
Lane 2 – OMZ175

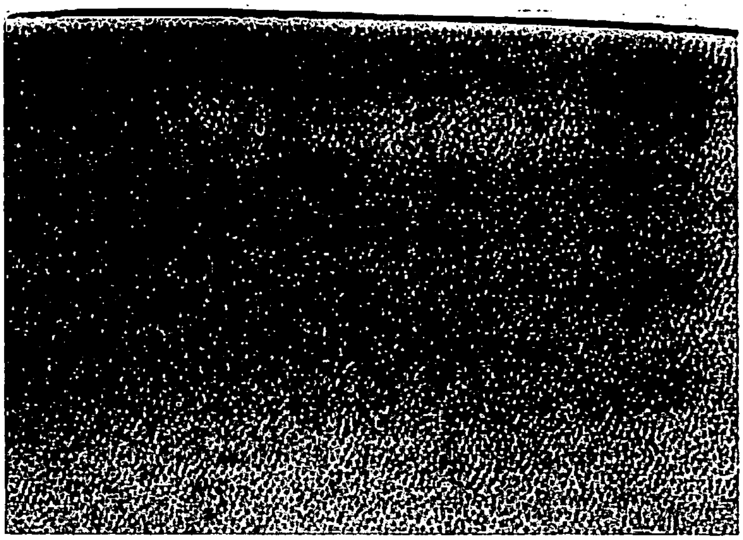
A32-2 peptidoglycan: Lane 3 – A32-2
Lane 4 – NG8
Lane 5 – SrtA-
Lane 6- OMZ175
Lane 7-UA159

Enzyme source

S.sobrinus peptidoglycan: Lane 8 - A32-2
S. gordonii peptidoglycan: Lane 9 – A32-2
S. oralis peptidoglycan: Lane 10 – A32-2

FIGURE 6A

Enzyme source:
NG8 A32-2 Marker



Peptidoglycan source: *Actinobacillus actinomycetemcomitans* 29522

FIGURE 6B

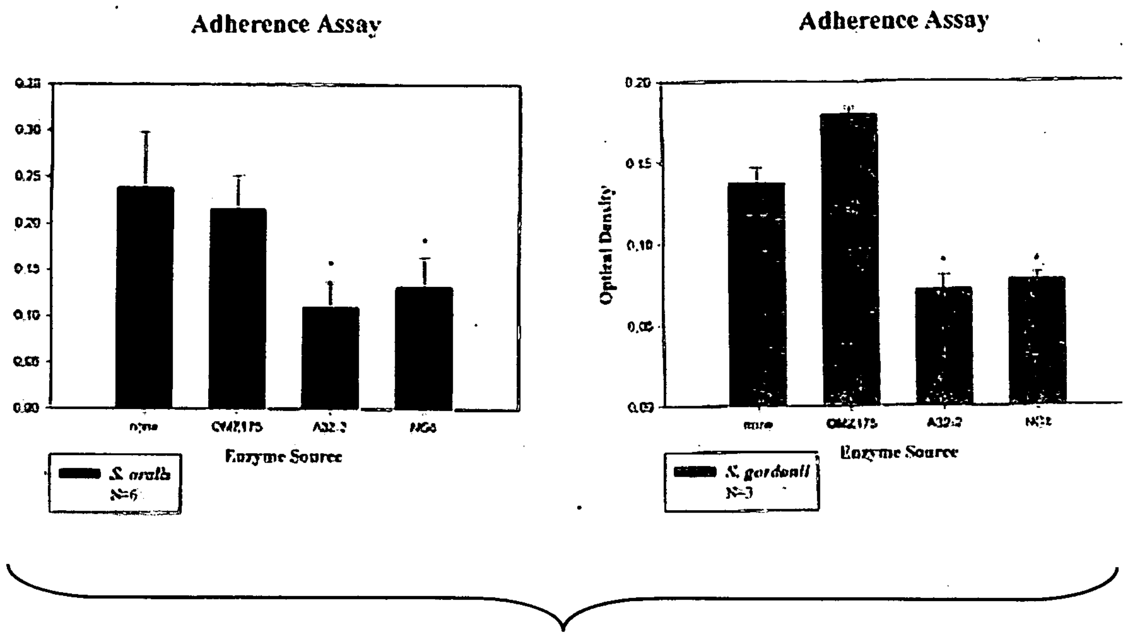

Adherence Assay
0.30
0.25
0.20
0.15
0.10
0.05
0.00
OMZ175
Enzyme Source
S. oralis
N=6
Adherence Assay
0.20
0.15
0.10
0.05
0.00
Optical Density
OMZ175
Enzyme Source
S. gordonii
N=3

FIGURE 6C

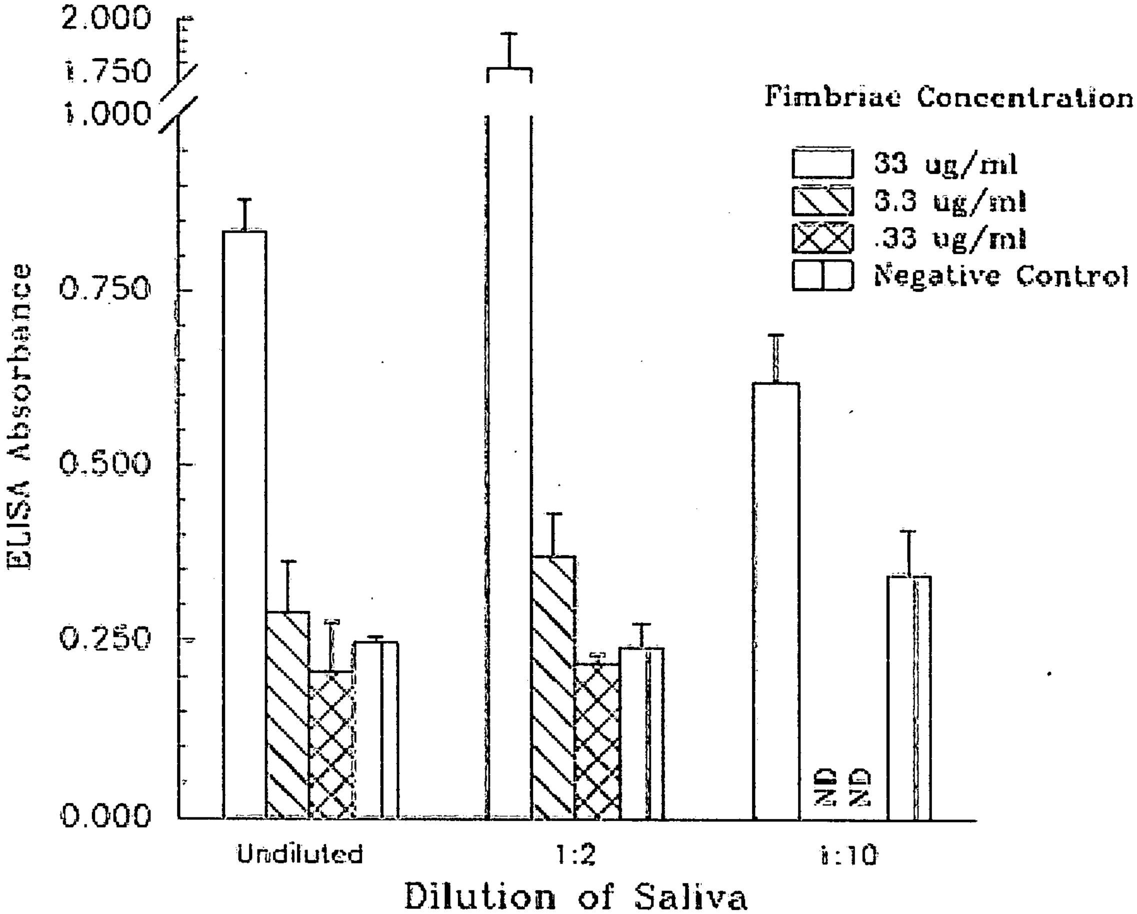

2.000
1.750
1.000
0.750
0.500
0.250
0.000
ELISA Absorbance
Fimbriae Concentration
33 ug/ml
3.3 ug/ml
.33 ug/ml
Negative Control
ND
ND
Undiluted
1:2
1:10
Dilution of Saliva

FIGURE 7

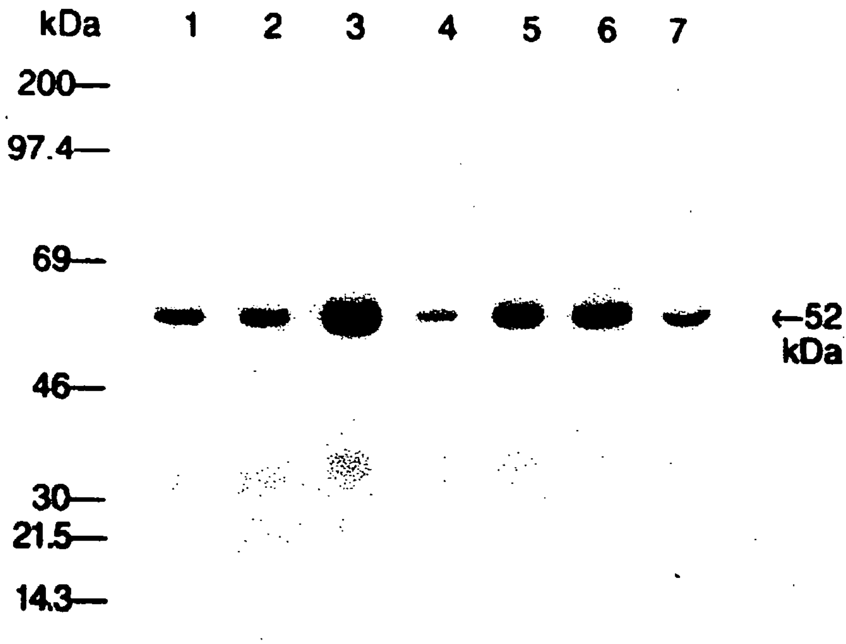


FIGURE 8

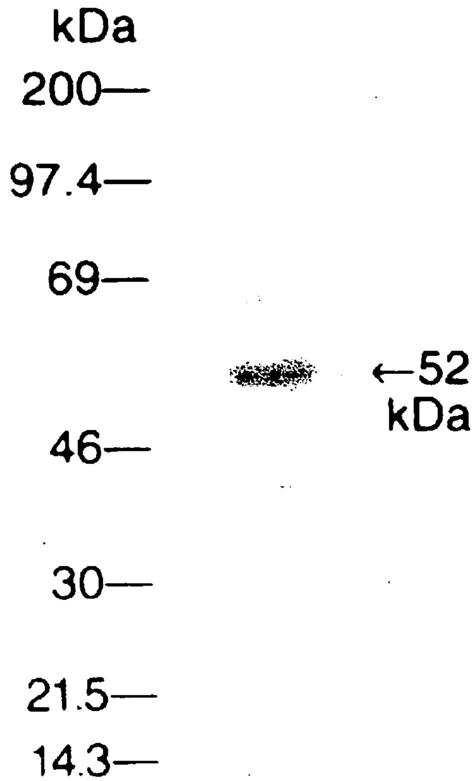
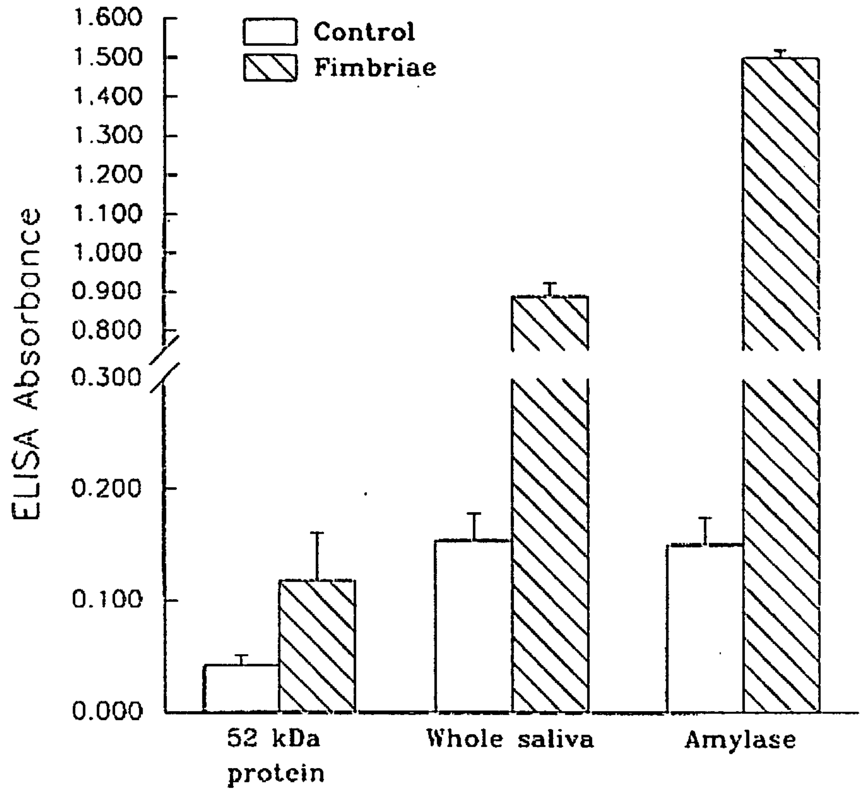


FIGURE 9



Control
Fimbriae
ELISA Absorbance
1.600
1.500
1.400
1.300
1.200
1.100
1.000
0.900
0.800
0.300
0.200
0.100
0.000
52 kDa protein
Whole saliva
Amylase

FIGURE 10

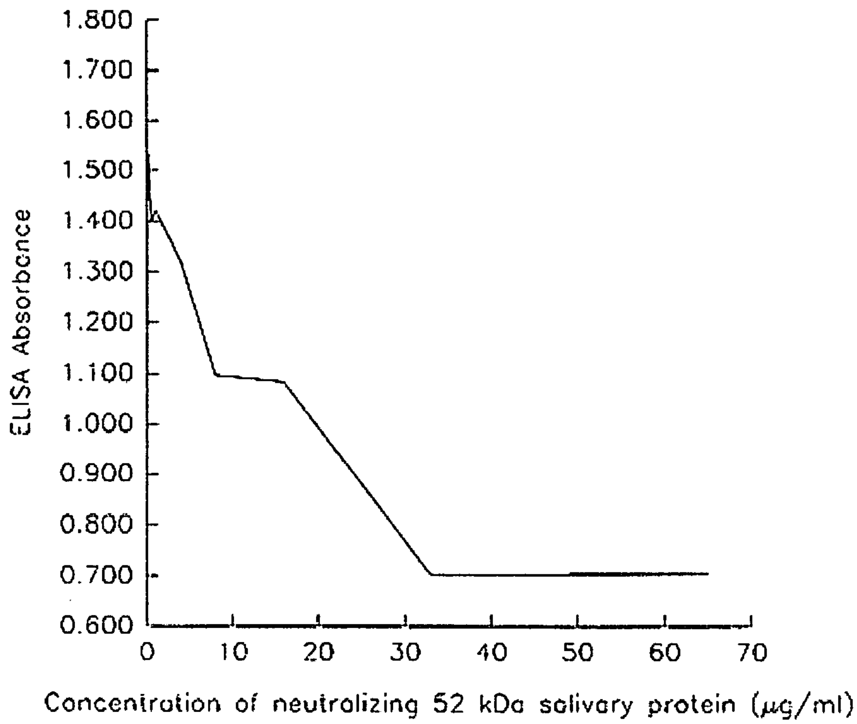

ELISA Absorbance
1.800
1.700
1.600
1.500
1.400
1.300
1.200
1.100
1.000
0.900
0.800
0.700
0.600
0
10
20
30
40
50
60
70
Concentration of neutralizing 52 kDa salivary protein (μg/ml)

FIGURE 11

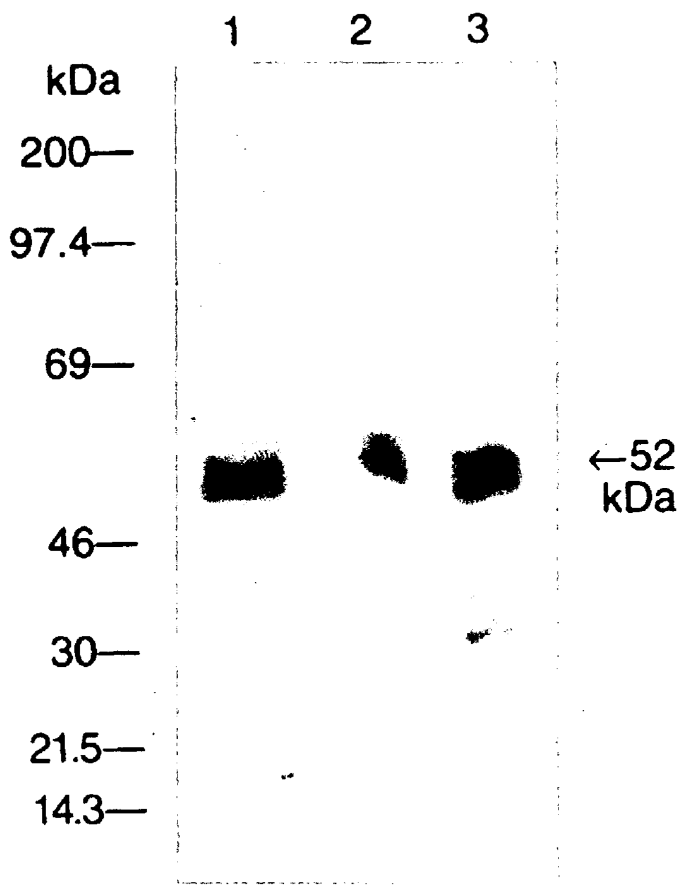


FIGURE 12